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January 2012; Revised September 2012

Dataset Integrity Check (DSIC) for the
TEDDY Data Files

Reference paper:

Hagopian WA, et al.
The Environmental Determinants of Diabetes in the Young (TEDDY): genetic criteria and international diabetes risk screening of 421 000 infants
Pediatric Diabetes 2011 May 12. [epub ahead of print]
doi: 10.1111/j.1399-5448.2011.00774.x

The TEDDY study seeks to identify environmental factors influencing the development of type 1 diabetes (T1D) via an intensive follow-up of children at elevated genetic risk. The study utilized a cost-effective yet accurate screening strategy to identify the high-risk cohort. The TEDDY cohort was identified through newborn screening via human leukocyte antigen (HLA) class II genes based on criteria established with pre-TEDDY data. TEDDY developed separate inclusion criteria for the general population (GP) and first-degree relatives (FDRs) of T1D patients. The FDR eligibility included nine haplogenotypes (*DR3/4*, *DR4/4*, *DR4/8*, *DR3/3*, *DR4/4b*, *DR4/1*, *DR4/13*, *DR4/9*, and *DR3/9*) for broad HLA diversity, while the GP eligibility included only the first four haplogenotypes with *DRB1*0403* as an exclusion allele. Screening for TEDDY has ended and the corresponding screening dataset has been archived at the NIDDK Repository.

As a partial check of the integrity of the archived TEDDY screening dataset, a dataset integrity check (DSIC) was performed to verify that selected published results from the TEDDY study can be reproduced using the archived dataset. The DSIC consists of a small number of analyses performed to duplicate published results reported by Hagopian WA, et al., in *Pediatric Diabetes* in May, 2011. Results of the DSIC are described below.

The intent of this DSIC is to provide confidence that the data distributed by the NIDDK repository is a true copy of the study data. Our intent is *not* to assess the integrity of the statistical analyses reported by study investigators. As with all statistical analyses of complex datasets, complete replication of a set of statistical results should not be expected on a first exercise in secondary analysis. This occurs for a number of reasons including differences in the handling of missing data, restrictions on cases included in samples for a particular analysis, software coding used to define complex variables, etc. Experience suggests that most discrepancies can ordinarily be resolved by consultation with the study data coordinating center (DCC), however this process is labor-intensive for both DCC and Repository staff. We do not attempt to resolve minor or inconsequential discrepancies with published results or discrepancies that involve complex analyses, *unless staff of the NIDDK Repository suspect that the observed discrepancy suggests that the dataset may have been corrupted in storage, transmission, or processing by repository staff*. We do, however, document in the integrity check those instances in which our secondary analyses produced results that were not fully consistent with those reported in the target publication.

Archived Dataset Contents. The DCC submitted a single *SAS* data file representing the raw data collected from the screening data collection form. The screening file is called <*teddy_screening.sas7bdat*>, dated 8/25/2011. The exact variables on the file are:

- <maskid>: Participant's masked ID number
- <hla_screen_genotype>: HLA screening genotype result (ineligible infants coded as "Not Eligible")
- <country>: Country of clinical center
- <anyfamilymemt1d>: indicator for whether the child has any family member with Type 1 diabetes
- <whichfamilymemt1d_father>: indicator for father having Type 1 diabetes
- <whichfamilymemt1d_mother>: indicator for mother having Type 1 diabetes
- <whichfamilymemt1d_sibling>: indicator for sibling having Type 1 diabetes.

DSIC Analysis Methods. For this DSIC, we attempted to replicate as many results as possible using the available screening variables.

First, the archived screening dataset was divided into two subpopulations, based on the variable <anyfamilymemt1d>:

1.) infants in the *general population* (GP)
2.) infants with a *first degree relative* with diabetes (FDR). [1]

Eligible subjects in the two subpopulations were identified by those testing positive for selected haplogenotypes. Infants with an FDR also had to test positive for any of nine haplogenotypes (*DR3/4, DR4/4, DR4/8, DR3/3,DR4/4b, DR4/1, DR4/13, DR4/9,* and *DR3/9*) for broad HLA diversity. Infants in the GP had to test positive for any of the first four haplogenotypes, with *DRB1*0403* as an exclusion allele. In the archived screening dataset, the variable <hla_screen_genotype> was used to determine each participant's eligibility status. [2]

Finally, the number screened, the number eligible, and breakdown of haplogenotypes were determined for each subpopulation, stratified by country of clinical center. Results were compared to published numbers.

All statistical analyses were conducted using *SAS version 9.2 (Cary, NC).*

[1] Per the DCC, all participants for whom <anyfamilymemt1d>='Yes' were considered as part of the FDR group; those with <anyfamilymemt1d>='No' or 'Unknown' were considered as part of the GP group. This was regardless of responses to <whichfamilymemt1d_father>, <whichfamilymemt1d_mother>, <whichfamilymemt1d_sibling>.
[2] Six participants in the screening dataset were missing their HLA screening result. The DCC confirmed that one of the participants was eligible (maskid=826749), while the other five were not.

DSIC Results. The publication reports that TEDDY screened a total of 414,714 GP infants from September 2004 to February 2010, of whom 19,906 (4.8%) were found to be eligible for follow-up studies. The archived screening dataset, current as of July 2011, indicates that 418,372 GP infants were screened, of whom 20,138 (4.8%) were eligible. The more recent date of the archived data likely explains the small increase in actual numbers (+1%), though the eligibility rate is exactly the same.

The publication reports that TEDDY screened a total of 6333 infants with an FDR, of whom 1,415 (22.3%) were found to be eligible. The archived screening dataset, current as of July 2011, indicates that 6,416 FDR infants were screened, of whom 1,433 (22.3%) were eligible. Again, the more recent date of the archived data likely explains the slight increase in actual numbers (+1%).

Table 1 is a comparison of archived versus published data for subpopulation breakdowns of number screened, number eligible, and percent eligible, by each country of screening. Country breakdowns show that the number of screened and number eligible are very similar between archived and published data. If anything, absolute numbers are slightly higher in archived data (corresponding to higher total numbers as presented above). The only exception is for GP infants screened in Sweden, where the number screened is slightly lower in archived versus published data; the eligibility rate, however, remains exactly the same.

Distributions by haplogenotype are also compared between archived and published data in Table 1. Distributions within each subpopulation are very similar between archived and published data; any differences were in the decimal points. As previously discussed, our analysis indicates that the population under study in archived data is slightly larger than that reported in the publication, which may explain these small differences.

Conclusion. With the replication of selected results, the analysis of archived screening data closely matches published results, allowing for variations from a possible increase in the number screened since publication. We are confident there were no errors in the transmission of the archived screening dataset from the DCC to the Repository.

Table 1: TEDDY human leukocyte antigen screening and eligiblity results for GP (Part 1) and FDR (Part 2) newborns, archived versus published data

Part 1. General Population (GP) Infants

Country	Screened (n)				Eligible (n)			Eligible (%)		
	Published	Archived	Diff, Arch - Pub	% Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub
USA*	273627	276809	3182	1%	11675	11871	196	4.3	4.3	0.0
FIN	59754	59876	122	0.2%	3370	3389	19	5.6	5.7	0.1
GER	34218	34570	352	1%	1353	1374	21	4.0	4.0	0.0
SWE	47115	47117	2	0.004%	3508	3504	-4	7.4	7.4	0.0
Total	**414714**	**418372**	**3658**	**1%**	**19906**	**20138**	**232**	**4.8**	**4.8**	**0.0**

Country	Haplogenotype Percent of Screened GP											
	A (DR 3/4)			B (DR 4/4)			C (DR 4/8)			D (DR 3/3)		
	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub
USA*	1.5-2.0	1.7	n.c.	0.6-1.4	0.9	n.c.	0.4-1.2	0.7	n.c.	0.9-1.0	1.0	n.c.
FIN	1.9	1.9	0.0	1.0	1.0	0.0	1.9	1.9	0.0	0.9	0.9	0.0
GER	1.7	1.7	0.0	0.7	0.7	0.0	0.4	0.4	0.0	1.1	1.1	0.0
SWE	3.2	3.2	0.0	1.6	1.6	0.0	1.0	1.0	0.0	1.7	1.6	-0.1
Total	**1.9**	**1.9**	**0.0**	**1.0**	**1.0**	**0.0**	**0.9**	**0.9**	**0.0**	**1.1**	**1.1**	**0.0**

Country	Haplogenotype Percent of Eligible GP											
	A (DR 3/4)			B (DR 4/4)			C (DR 4/8)			D (DR 3/3)		
	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub
USA*	**35.2-44.2**	39.7	n.c.	18.0-24.6	20.4	n.c.	11.0-21.3	16.1	n.c.	18.9-26.7	23.8	n.c.
FIN	33.6	33.5	-0.1	17.7	17.6	-0.1	32.7	32.8	0.1	16.0	16.0	0.0
GER	43.8	43.9	0.1	18.8	18.8	0.0	10.6	10.6	0.0	26.9	26.7	-0.2
SWE	42.5	42.6	0.1	21.7	21.7	0.0	13.6	13.6	0.0	22.2	22.2	0.0
Total	**39.5**	**39.5**	**0.0**	**20.0**	**20.0**	**0.0**	**18.1**	**18.1**	**0.0**	**22.4**	**22.4**	**0.0**

* published as 3 clinical centers: COL, GEO, and WAS

Table 1, continued: TEDDY human leukocyte antigen screening and eligiblity results for GP (Part 1) and FDR (Part 2) newborns, archived versus published data.

Part 2, First Degree Relative (FDR) infants

Country	Screened (n)				Eligible (n)			Eligible (%)		
	Published	Archived	Diff, Arch - Pub	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub
USA**	2872	2930	58	2%	615	624	9	21.4	21.3	-0.1
FIN	924	928	4	0.4%	288	290	2	31.2	31.3	0.1
GER	1518	1535	17	1%	297	300	3	19.6	19.5	-0.1
SWE	1019	1023	4	0.4%	215	219	4	21.1	21.4	0.3
Total	**6333**	**6416**	**83**	**1%**	**1415**	**1433**	**18**	**22.3**	**22.3**	**0.0**

Country	Haplogenotype Percent of Eligible FDR											
	A (DR 3/4)			B (DR 4/4)			C (DR 4/8)			D (DR 3/3)		
	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub
USA**	29.5-50.0	35.3	n.c.	0.0-17.1	15.9	n.c.	0.0-12.5	6.7	n.c.	15.7-33.3	16.3	n.c.
FIN	20.8	20.7	-0.1	14.2	14.5	0.3	13.9	14.1	0.2	5.6	5.5	-0.1
GER	31.6	31.7	0.1	15.2	15.0	-0.2	6.7	6.7	0.0	12.8	13.3	0.5
SWE	33.5	33.3	-0.2	20.5	21.0	0.5	7.9	8.2	0.3	11.6	11.9	0.3
Total	**31.5**	**31.3**	**-0.2**	**15.6**	**16.2**	**0.6**	**8.5**	**8.4**	**-0.1**	**12.7**	**12.8**	**0.1**

Country	Haplogenotype Percent of Eligible FDR (continued)											
	E (DR 4/4b)			F (DR 4/1)			G (DR 4/13)			H (DR 4/9)		
	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub	Published	Archived	Diff, Arch - Pub
USA**	0.0-1.4	0.8	n.c.	0.0-17.1	15.9	n.c.	0.0-6.2	5.1	n.c.	0.0-1.9	1.1	n.c.
FIN	0.0	0.0	0.0	29.2	28.9	-0.3	5.9	5.9	0.0	6.9	6.9	0.0
GER	0.3	0.3	0.0	22.6	22.3	-0.3	7.1	7.0	-0.1	1.3	1.3	0.0
SWE	0.5	0.5	0.0	16.7	16.4	-0.3	7.0	6.8	-0.2	1.4	1.4	0.0
Total	**0.5**	**0.5**	**0.0**	**20.1**	**20.0**	**-0.1**	**6.0**	**5.9**	**-0.1**	**2.4**	**2.4**	**0.0**

Country	Haplogenotype Percent of Eligible FDR (continued)		
	I (DR 3/9)		
	Published	Archived	Diff, Arch - Pub
USA**	0.0-3.8	2.9	n.c.
FIN	3.5	3.4	-0.1
GER	2.4	2.3	-0.1
SWE	0.9	0.5	-0.4
Total	**2.6**	**2.5**	**-0.1**

** Tabulations for USA represent a combination of 5 clinical centers: COL, GEO, WAS, NBD, CHP

References

[1] Hagopian WA, Erlich H, Lernmark Å, Rewers M, Ziegler AG, Simell O, Akolkar B, Vogt Jr R, Blair A, Ilonen J, Krischer J, She J, and the TEDDY Study Group. The Environmental Determinants of Diabetes in the Young (TEDDY): genetic criteria and international diabetes risk screening of 421 000 infants.
Pediatric Diabetes 2011 May 12. [Epub ahead of print]

Appendices

[1] SAS version 9.2 Log for programming code submitted for the replication of results in *Hagopian WA, et al, Pediatric Diabetes 2011 May 12*

[2] SAS version 9.2 Output for programming code submitted for the replication of results in *Hagopian WA, et al, Pediatric Diabetes 2011 May 12*

Appendix 1

SAS version 9.2 Log
for programming code submitted
for the replication of results in
Hagopian WA, et al., Pediatric Diabetes 2011 May 12.

```
NOTE: Copyright (c) 2002-2008 by SAS Institute Inc., Cary, NC, USA.
NOTE: SAS (r) Proprietary Software 9.2 (TS2M0)
      Licensed to RTI INTL MAIN, Site 70006746.
NOTE: This session is executing on the XP_PRO  platform.



NOTE: SAS initialization used:
      real time           8.62 seconds
      cpu time            2.43 seconds

1    options ps=55 ls=75 nonumber formchar='|----|+\---+=|-^<>*' mprint
orientation=portrait;
2
3    ********************************************************
4    * TEDDY dsic for submission.sas                        *
5    * Purpose:  to perform Data Set Integrity Analyses     *
6    * on TEDDY the Screening legacy dataset                *
7    *                                                      *
8    *                                                      *
9    * Input:                                               *
10   * teddy_screening.sas7bdat, submitted by TEDDY study group *
11   *           dated 8/25/2011                            *
12   *                                                      *
13   *                                                      *
14   * comparison study paper:                              *
15   * Hagopian WA, et al... Pediatric Diabetes 2011 May 12.    *
16   *                                                      *
17   * Programmed by: S. Tan                                *
18   ********************************************************;
19
20   libname teddy 'C:\Documents and Settings\stan\My
Documents\DATA\NIDDK\TEDDY\Teddy_DATA';
NOTE: Libref TEDDY was successfully assigned as follows:
      Engine:        V9
      Physical Name: C:\Documents and Settings\stan\My
Documents\DATA\NIDDK\TEDDY\Teddy_DATA
21
22   data teddyscreen; set teddy.teddy_screening;
NOTE: Data file TEDDY.TEDDY_SCREENING.DATA is in a format that is native to another
host, or the
      file encoding does not match the session encoding. Cross Environment Data
Access will be
      used, which might require additional CPU resources and might reduce
performance.
23
24     elig=.;
25     if hla_screen_genotype in ('Not*Eligible','') then elig=0;
26        /* confirmed in email sent by TEDDY DCC 10/17/11 */
27     else if hla_screen_genotype^='' then elig=1;
28     IF MASKID=826749 THEN ELIG=1;
29        /* mask ID identified in email sent by TEDDY DCC 10/17/11 */
30
31     if anyfamilymemt1d='Yes' then group='T1D';
32     else if anyfamilymemt1d in ('No','Unknown') then group='GP';
33
34     * general population *;
35     title GP, eligibility rate;
```

```
NOTE: There were 424788 observations read from the data set TEDDY.TEDDY_SCREENING.
NOTE: The data set WORK.TEDDYSCREEN has 424788 observations and 9 variables.
NOTE: DATA statement used (Total process time):
      real time           11.53 seconds
      cpu time            1.76 seconds


36   proc freq; tables country*elig/ missing; where group='GP'; run;

NOTE: There were 418372 observations read from the data set WORK.TEDDYSCREEN.
      WHERE group='GP';
NOTE: PROCEDURE FREQ used (Total process time):
      real time           0.85 seconds
      cpu time            0.50 seconds


37     title GP, haplogenotype distn among all screened;
38   proc freq; tables country*hla_screen_genotype/ missing; where group='GP'; run;

NOTE: There were 418372 observations read from the data set WORK.TEDDYSCREEN.
      WHERE group='GP';
NOTE: PROCEDURE FREQ used (Total process time):
      real time           0.26 seconds
      cpu time            0.26 seconds


39     title GP, haplogenotype distn among all eligible;
40   proc freq; tables country*hla_screen_genotype/ missing; where group='GP' and
elig=1; run;

NOTE: There were 20138 observations read from the data set WORK.TEDDYSCREEN.
      WHERE (group='GP') and (elig=1);
NOTE: PROCEDURE FREQ used (Total process time):
      real time           0.18 seconds
      cpu time            0.17 seconds


41
42     * infants with a relative with T1D *;
43     title T1D, eligibility rate;
44   proc freq; tables country*elig/ missing; where group='T1D'; run;

NOTE: There were 6416 observations read from the data set WORK.TEDDYSCREEN.
      WHERE group='T1D';
NOTE: PROCEDURE FREQ used (Total process time):
      real time           0.06 seconds
      cpu time            0.04 seconds


45     title T1D, haplogenotype distn among all eligible;
46   proc freq; tables country*hla_screen_genotype/ missing; where group='T1D' and
elig=1; run;

NOTE: There were 1433 observations read from the data set WORK.TEDDYSCREEN.
      WHERE (group='T1D') and (elig=1);
NOTE: PROCEDURE FREQ used (Total process time):
      real time           0.06 seconds
```

Appendix 2

SAS version 9.2 Output
for programming code submitted
for the replication of results in
Hagopian WA, et al., Pediatric Diabetes 2011 May 12.

The FREQ Procedure

Table of country by elig

country(Country of Clinical Center)
elig

Frequency Percent Row Pct Col Pct	0	1	Total
Finland	56487 13.50 94.34 14.18	3389 0.81 5.66 16.83	59876 14.31
Germany	33196 7.93 96.03 8.34	1374 0.33 3.97 6.82	34570 8.26
Sweden	43613 10.42 92.56 10.95	3504 0.84 7.44 17.40	47117 11.26
US	264938 63.33 95.71 66.53	11871 2.84 4.29 58.95	276809 66.16
Total	398234 95.19	20138 4.81	418372 100.00

The FREQ Procedure

Table of country by hla_screen_genotype

country(Country of Clinical Center)
hla_screen_genotype(HLA screening genotype)

Frequency Percent Row Pct Col Pct	DR3*0501/0201*DR3*0501/0201	DR4*030X/0302*DR3*0501/0201	DR4*030X/0302*DR4*030X/0302	DR4*030X/0302*DR8*0401/0402	Not*Eligible	Total
Finland	3 0.00 0.01 50.00	543 0.13 0.91 12.03	1136 0.27 1.90 14.29	598 0.14 1.00 14.81	1111 0.27 1.86 30.51	56485 13.50 94.34 14.18	59876 14.31
Germany	0 0.00 0.00 0.00	367 0.09 1.06 8.13	603 0.14 1.74 7.59	258 0.06 0.75 6.39	146 0.03 0.42 4.01	33196 7.93 96.03 8.34	34570 8.26
Sweden	0 0.00 0.00 0.00	777 0.19 1.65 17.22	1491 0.36 3.16 18.76	761 0.18 1.62 18.85	475 0.11 1.01 13.05	43613 10.42 92.56 10.95	47117 11.26
US	3 0.00 0.00 50.00	2825 0.68 1.02 62.61	4717 1.13 1.70 59.36	2420 0.58 0.87 59.95	1909 0.46 0.69 52.43	264935 63.33 95.71 66.53	276809 66.16
Total	6 0.00	4512 1.08	7947 1.90	4037 0.96	3641 0.87	398229 95.19	418372 100.00

The FREQ Procedure

Table of country by hla_screen_genotype

country(Country of Clinical Center)
hla_screen_genotype(HLA screening genotype)

Frequency Percent Row Pct Col Pct		DR3*0501/0201*DR3*0501/0201	DR4*030X/0302*DR3*0501/0201	DR4*030X/0302*DR4*030X/0302	DR4*030X/0302*DR8*0401/0402	Total
Finland	1	543	1136	598	1111	3389
	0.00	2.70	5.64	2.97	5.52	16.83
	0.03	16.02	33.52	17.65	32.78	
	100.00	12.03	14.29	14.81	30.51	
Germany	0	367	603	258	146	1374
	0.00	1.82	2.99	1.28	0.72	6.82
	0.00	26.71	43.89	18.78	10.63	
	0.00	8.13	7.59	6.39	4.01	
Sweden	0	777	1491	761	475	3504
	0.00	3.86	7.40	3.78	2.36	17.40
	0.00	22.17	42.55	21.72	13.56	
	0.00	17.22	18.76	18.85	13.05	
US	0	2825	4717	2420	1909	11871
	0.00	14.03	23.42	12.02	9.48	58.95
	0.00	23.80	39.74	20.39	16.08	
	0.00	62.61	59.36	59.95	52.43	
Total	1	4512	7947	4037	3641	20138
	0.00	22.41	39.46	20.05	18.08	100.00

The FREQ Procedure

Table of country by elig

country(Country of Clinical Center)
elig

Frequency Percent Row Pct Col Pct	0	1	Total
Finland	638 9.94 68.75 12.80	290 4.52 31.25 20.24	928 14.46
Germany	1235 19.25 80.46 24.78	300 4.68 19.54 20.94	1535 23.92
Sweden	804 12.53 78.59 16.13	219 3.41 21.41 15.28	1023 15.94
US	2306 35.94 78.70 46.28	624 9.73 21.30 43.55	2930 45.67
Total	4983 77.67	1433 22.33	6416 100.00

The FREQ Procedure

Table of country by hla_screen_genotype

country(Country of Clinical Center) hla_screen_genotype(HLA screening genotype)

Frequency Percent Row Pct Col Pct	DR3*0501 /0201*DR 3*0501/0 201	DR3*0501 /0201*DR 9*030X/0 303	DR4*030X /0302*DR 1*0101/0 501	DR4*030X /0302*DR 13*0102/ 0604	DR4*030X /0302*DR 3*0501/0 201	DR4*030X /0302*DR 4*030X/0 20X	DR4*030X /0302*DR 4*030X/0 302	DR4*030X /0302*DR 8*0401/0 402	DR4*030X /0302*DR 9*030X/0 303	Total
Finland	16	10	84	17	60	0	42	41	20	290
	1.12	0.70	5.86	1.19	4.19	0.00	2.93	2.86	1.40	20.24
	5.52	3.45	28.97	5.86	20.69	0.00	14.48	14.14	6.90	
	8.70	27.78	29.37	20.00	13.39	0.00	18.10	33.88	58.82	
Germany	40	7	67	21	95	1	45	20	4	300
	2.79	0.49	4.68	1.47	6.63	0.07	3.14	1.40	0.28	20.94
	13.33	2.33	22.33	7.00	31.67	0.33	15.00	6.67	1.33	
	21.74	19.44	23.43	24.71	21.21	14.29	19.40	16.53	11.76	
Sweden	26	1	36	15	73	1	46	18	3	219
	1.81	0.07	2.51	1.05	5.09	0.07	3.21	1.26	0.21	15.28
	11.87	0.46	16.44	6.85	33.33	0.46	21.00	8.22	1.37	
	14.13	2.78	12.59	17.65	16.29	14.29	19.83	14.88	8.82	
US	102	18	99	32	220	5	99	42	7	624
	7.12	1.26	6.91	2.23	15.35	0.35	6.91	2.93	0.49	43.55
	16.35	2.88	15.87	5.13	35.26	0.80	15.87	6.73	1.12	
	55.43	50.00	34.62	37.65	49.11	71.43	42.67	34.71	20.59	
Total	184	36	286	85	448	7	232	121	34	1433
	12.84	2.51	19.96	5.93	31.26	0.49	16.19	8.44	2.37	100.00